

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Kun On: October 5, 2002, 03:30:35 ; Search time 1713.89 Seconds
(without alignments)
3709.145 Million cell updates/sec

Title: US-09-525-361A-23
Perfect score: 471
Sequence: 1 cttgaagcattttgtctg.....aactatgagcgagctaacaat 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID Description
1	431.8	91.7	436 10 W72837 W72837 zd57g12.r1
2	403.2	85.6	432 10 W72838 W72838 zd57g12.s1
3	390.8	83.0	420 9 AW070916 AW070916 xa31d01.x
4	388.6	82.5	423 10 BF742809 BF742809 IL2-BT080
5	379	80.5	402 9 A1139456 A1139456 qc20g01.x
6	345.2	73.3	454 10 BG202312 BG202312 RST21668
7	331	70.3	376 10 BG218084 BG218084 RST37810
8	316.8	67.3	345 9 BE092421 BE092421 CM1-BT073
9	309.8	65.8	391 10 BG185269 BG185269 RST4208 A
10	308.8	65.6	403 10 R75793 R75793 y121f09.r1
11	301.4	64.0	314 12 A2694036 A2694036 AST-2H8BG
12	299.2	63.5	343 10 BG202313 BG202313 RST21669
13	294	62.4	313 9 AW176044 AW176044 QVO-BT010
14	289.4	61.4	294 9 AA340069 AA340069 EST45219
15	281	59.7	316 9 BE186013 BE186013 CM1-HT073
16	281	59.7	316 10 BE926938 BE926938 CM1-BT073
17	255.8	54.3	443 9 A1127172 A1127172 qb99a08.x

18	247.6	52.6	308	9	A1905687	A1905687	1L-R-BT095-
19	217.8	46.2	251	10	BC197186	BC197186	RS116A24
20	202.8	43.1	221	9	BE074512	BE074512	1L5-BT057
21	197.8	42.0	462	9	AW294149	AW294149	UI-H-BT2-
22	197	41.8	224	9	AW291950	AW291950	UI-H-BT2-
23	196.6	41.7	230	10	BE815819	BE815819	PM3-BN017
24	187.8	39.9	248	10	BE815824	BE815824	PM3-BN017
25	159	33.8	193	9	A1905624	A1905624	CM-BT094-
26	154	32.7	224	9	A1905837	A1905837	CM-BT094-
27	151	32.1	211	10	BC183176	BC183176	1L-BT099-
28	150	31.8	212	10	BC192597	BC192597	RST2047 A
29	149.4	31.7	178	9	A1905623	A1905623	CM-BT094-
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31	133	28.2	136	9	A1905633	A1905633	CM-BT094-
32	102.8	21.8	224	10	BE815853	BE815853	PM3-BN017
33	85	18.0	498	10	BI279448	BI279448	UI-R-DA0-
34	83	17.6	536	10	BI339750	BI339750	364820 MA
35	82.6	17.5	572	10	BF080542	BF080542	231581 MA
36	82.4	17.5	490	10	BI279279	BI279279	UI-R-DA0-
37	82.4	17.5	492	10	BI279431	BI279431	UI-R-DA0-
38	82.4	17.5	499	10	BI279473	BI279473	UI-R-DA0-
39	81.8	17.4	486	10	BI282803	BI282803	UI-R-DA0-
40	80.8	17.2	481	10	BI279272	BI279272	UI-R-DA0-
41	80.8	17.2	490	10	BI279159	BI279159	UI-R-DA0-
42	80.8	17.2	493	10	BI279513	BI279513	UI-R-DA0-
43	80.8	17.2	493	10	BI279518	BI279518	UI-R-DA0-
44	80.8	17.2	495	10	BI279214	BI279214	UI-R-DA0-
45	80.8	17.2	496	10	BI279121	BI279121	UI-R-DA0-

ALIGNMENTS

RESULT 1

LOCUS W72837

DEFINITION zd57g12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone, IMAGE:344806 5', similar to contains element MER40 repetitive element ; mRNA sequence.

ACCESSION W72837

VERSION W72837.1

KEYWORDS GI:1382813

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 436)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL: contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 508 Std Error: 0.00

Seq primer: mob.REGA+ET.

Location/Qualifiers

1. 436

/organism="Homo sapiens"

/db_xref="GDB:1270181"

/db_xref="taxon:9606"

/clone_lib="IMAGE:344806"

/sex="unknown"

/lab_host="DH10B (ampicillin resistant)"


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DEFINITION similar to contains element TAK1 repetitive element ;, mRNA
sequence.
ACCESSION AW070916 GI:6025914
VERSION AW070916.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 420)
NCI-CCAP http://www.nci.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cuaphs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www-ilo.lilni.gov/ubrp/image/image.html
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/lab_host="DH108"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: Not; Cloned unidirectionally. Primer: Oligo dT.
library constructed by Life Technologies."
BASE COUNT 119 a 76 c 116 g 109 t
ORIGIN
source
Query Match 83.0%; Score 390.8; DB 9; Length 420;
Best Local Similarity 98.1%; Pred. No. 2.8e-90;
Matches 406; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 57 tagcagtcctggtaactcttggagattccatcttctcgtctcctcaccgaatccgacaa 116
DB 420 TAGCAGTCCTGGTACTCTTGGGAGTTTCCATCTTCTGCTCTGCTCCACAAATCCGACAA 361
QY 117 cagctctccagctgacagatctcagactactgctcgtcgtgatgatgaagccctctgag 176
DB 360 CAGCTGCTCAGCTGACACGATCCAGCTACTGCTCTGCTGATGATGAAGCCCTGATG 301
QY 177 ctgaagaccactgctgctgaacactgacactgctcctcactgcaaccacccg 236
DB 100 CTGAAGACCACCTGCTGTGCAACCACTGCGACCACTGCTGCTCTACCACTGCAACCCG 241
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DB 240 CTGCTTCTACCACTGCTGTAAGACATTCACGTTTACCCAAATGGGTGGGATCTCC 181
QY 297 cgaatggtagagtgctcctcctgagatgggaatcagrtttagctctctcgaatgggtccaa 356
DB 180 GCAATGGTAGAGTGTCTCCCTCAGATGGAATCAGCTTGAGTCTCTTCGCAATT-GGTCACA 122
QY 357 actattcactgctcctgctgatttcatccaaactacttaactctgctacgataccctttaa 416
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Db 121 ACTATTTCATGCTTCCTCTGATTTTCATCCAACTACTTACTTGCCTACCATATCCCTTTTAA 62
QY 417 tctcgaatcagttatttcttccaaataaaataactatgaagcgaacta 470
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RESULT 4
LOCUS BF742809 423 bp mRNA linear EST 10 JAN 2001
DEFINITION IL2-BT0807-041000-176-G03 BT0807 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF742809
VERSION BF742809.1 GI:12069485
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. K.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,
Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare
M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?LI=IL2612 IL2-BT0807-
041000-176-G03&t3-2000-10-04&l4=1)
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High quality sequence stop: 421.
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/note="Organ: breast; Vector: puc18; Site_1: Sma1; Site_2:
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from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 89 a 123 c 87 g 124 t
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Matches 402; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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DB 15 CTTTGAAGCATTTTGTCTGTGCTCCCTGATCTTCAGTCCACCACCATGAAGTCTTACG 74
QY 61 aatcctcgtactcttgggaatttccatcttcttggtctctgcccagaatccgacaacagc 120
DB 75 AGTCTGTGTTCTTGGGAGTTTCCATCTTCTGCTCTGCTCCAGAAATCCGACAACAGC 134
QY 121 tgcctcagctgacacgtatccacgtactcgtcctcgtgatgatgaagccctgatgctga 180

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Query Match		73.3%;	Score 345.2;	DB 10;	Length 464;
Best Local Similarity		97.6%;	Pred. No. 1.6e-78;		
Matches 161;		Conservative 0;	Mismatches 8;	Indels 1;	Gaps 1;
QY	101	grrccuagatccgagaaacagctgctccaaactacacgtatccagctactcggctccctgctgctgat			
DB	89	GACAGAAATCCGACAAACAGCTGCTCCAGCTGACACAGTATCCAGCTACTGCTCTGAT			
QY	161	gataaagccctgagatgctgaaarrractgctgctgacaaacactcagacactgctgctctct			
DB	149	GATGAAGCCCTTGATGCTGAAACCACTTCCTGCTGCAACCACTGCGACCACTGCTGCTCT			
QY	221	acccctgaaacacccgctgctcttaccacactcgtgtaaaacacattccagttttaccraaa			
DB	204	ACCACTGCAACCAACCGCTGCTCTTACCACAGCTGCTGAAGACATTCAGTTTACCACAA			
QY	281	taqatltgnggatctccccaatggtgaaagctgctgctccctgaagatggaatcagcttgagctct			
DB	264	tGGAATGAGGATCTCCGCAATCGTAGAGCTGTCGCTGAGATGCAATCAGCTTCAGTCTT			
QY	341	ctacatlttqgtcaccactattcagcttcctctgctgctgctgctgctgctgctgctgctgct			
DB	329	CTCAATTTGGTACAACTATTCATGCTTCTGTCATTTTCATTCATTCATTCATTCATTCAT			
QY	401	taccatctccctcttctcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct			
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QY	461	cgaactaaca 470			
DB	448	CAACAAAAA 457			
RESULT 7					
LOCUS HG218084 376 bp mRNA linear EST 21-APR-2001					
DEFINITION RST37810 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.					
ACCESSION BG218084					
VERSION BG218084.1 GI:13744105					
KEYWORDS EST.					
SOURCE human.					
ORGANISM Homo sapiens					
REFERENCE: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS Hartington, J.J., Sheri, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McEligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.					
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression					
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)					
MEDLINE 21227151					
COMMENT Contact: Scott J. Cain					
Athersys, Inc.					
3201 Carnegie Ave, Cleveland, OH 44115, USA					
Tel: 216 431 9900					
Fax: 216 361 9596					
Email: scaine@atersys.com					
High quality sequence stop: 376.					
Location/Qualifiers					
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/clone_lib="Athersys RAGE Library"					
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FEATURES source					
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QY	164	gaagcccttgatgctgaaacrractgctgctgaaacacactgacacactgctgctgctgctgct			
DB	64	GAAGCCTCTGATGCTGAAACCACTGCTGCTGCTGCAACCACTGCGACCACTGCTGCTCTAT			
QY	224	actgcaaacacccgctgcttctcaacactgctcgtaagacacattccagttttaccraaatga			
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QY	284	gttgaggatctccccaatggtgaaagctgctgctgctgctgctgctgctgctgctgctgctg			
DB	184	GTTGGGATCTCCGCAATCGTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT			
QY	344	caattgggtcacaactcattcattcctgctgctgctgctgctgctgctgctgctgctgctg			
DB	244	CAATT-CGTACAACTATTTCATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT			
QY	404	gatatcccttctctctcattcattcattcattcattcattcattcattcattcattcattcatt			
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ACCESSION BE092421					
VERSION BE092421.1 GI:8482977					
KEYWORDS EST.					
SOURCE human.					
ORGANISM Homo sapiens					
REFERENCE: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.					
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags					
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)					
MEDLINE 20202663					
COMMENT Contact: Simpson A.J.G.					
Laboratory of Cancer Genetics					
Ludwig Institute for Cancer Research					
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil					
Tel: +55-11-2704922					
Fax: +55-11-2707001					
Email: asimpson@ludwig.org.br					
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL					
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-cm1-BT0738-250					
400-200-cl2&t3=2000-04-25&t4=1)					
Seq primer: puc 18 forward					

GSS.
 human.
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 314)
 AUTHORS
 Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A.,
 Durick,K. and Pollok,B.
 TITLE
 Exon-trap tags from a HL-60 GenomeScreen(TM) Library
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: greg.henkel
 Gene Expression
 Aurora Biosciences Corp.
 11010 Torreyana Road, San Diego, CA 92121, USA
 Tel: 8584048436
 Fax: 8584046719
 Email: henkelg@aurorabio.com
 Pools of cells were isolated from a GenomeScreen(TM) library. The
 library of cells was generated by retroviral integration of a gene
 tagging element consisting of: 1) A promoterless beta-lactamase
 preceded by a splice acceptor as a reporter for gene expression;
 2) A promoter driving neomycin resistance followed by a splice
 donor to trap downstream exons. 3' RACE from neomycin gene was
 performed using total RNA from isolated pools. Output was shotgun
 cloned in pAmp-1 and used to transform DH5-alpha competent
 bacteria. 5' ends of reported sequences were immediately preceded
 by splice donor from the trapping construct.
 Class: exon-trapped.

FEATURES	Causes: Contaminated.									
source	Location/Qualifiers									
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	/cell_type="promyeloblast"									
	/cell_line="HL-60"									
	/note="Organ: peripheral blood; Vector: pAmp-1; 1' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and used to transform DH5-alpha competent bacteria."									
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ORIGIN										
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Db	1	CTGTCTCTGTGATGATGAAGCCCTTGATGCTGAACCACTGCTGCTGAACCACTCGCA	60							
Qy	207	ccactgctgctctaccactgcaaccacccgctgctctaccactgctcgtaaagacattc	266							
Db	61	CCACTGTGCTCTTACCACCTGCAACCAACCCGCTGTTCTACCACTGCTCGTAAACACATTC	120							
Qy	267	cagttttaccaccaatgggttggggatgcccgaaatggtagtgctccctgagatggaa	326							
Db	121	CAGTTTACCACCAATGGGTTGGGGATGCTCCCGAATGGTAGTGTGCTCGATCGAA	180							
Qy	327	tcagcttgagctctctgcaattgggtcaccaactatcatgctccctgctgattccatccaa	386							
Db	181	TCAGCTTGAGTCTTCTGCAATT-GGTCAACAATATTATGCTTCCTGATTCATCCAA	239							
Qy	387	ctacttaccttgctcaagataatcccttttatctctaatcagtttatcttcttcaataa	446							
Db	240	CTACTTACCCTTGCTACGATATCCCCCTTATCTCTAATCAGTTTATTTCTTTCAATAA	299							
Qy	447	aaataactatgagc	461							
Db	300	AAAAAATATGAGC	314							

47
507
240
Db

CTACTTACCTTGCCAGGATATCCCCCTTTATCTCTAAATCAGTTTATTTCCTTCANATAA

461
Qy

aaaataactatgagc

314
Db

AAAATAACTATGAGC

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 03:59:20 ; Search time 46.3 Seconds
(without alignments)
2498.777 Million cell updates/sec

Title: US-09-525-361A-23
Perfect score: 471
Sequence: 1 ctttgaagcattttgtctgtg.....aactatgagcagctaacat 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448.4	95.2	497	4	US-09-247-155-41
2	68.6	14.6	397	3	US-09-253-691-3
3	65.4	13.9	477	4	US-09-135-994-1
4	65	13.8	234	1	US-08-469-802B-3
5	65	13.8	234	2	US-08-267-803B-3
6	64.8	13.8	3376	1	US-08-320-559-29
7	64.8	13.8	3376	3	US-08-545-860D-29
8	64.8	13.8	3376	5	PCT-US94-04496-29
9	64.6	13.7	203	4	US-09-043-303-7
10	63.4	13.5	168	1	US-08-469-802B-4
11	63.4	13.5	168	2	US-08-267-803B-4
12	63.4	13.5	171	1	US-08-469-802B-5
13	63.4	13.5	171	2	US-08-267-803B-5
14	63.4	13.5	195	1	US-08-469-802B-2
15	63.4	13.5	195	2	US-08-267-803B-2
16	62.8	13.3	154	1	US-08-469-802B-6
17	62.8	13.3	154	2	US-08-267-803B-6
18	62.2	13.2	165	4	US-09-043-303-17
19	52.6	11.2	2580	3	US-09-050-863-2
20	52.6	11.2	2580	4	US-09-359-081-2
21	52.6	11.2	3489	2	US-08-728-323A-1
22	52.6	11.2	5452	2	US-09-130-114-1
23	52.6	11.2	9600	4	US-08-910-647-1
24	52.6	11.2	10596	1	US-07-884-811-15
25	52.6	11.2	10596	1	US-07-885-971-15
26	52.6	11.2	10596	1	US-08-087-763A-15
27	52.6	11.2	10596	1	US-08-194-088B-15

C 28	52.6	11.2	10596	2	US-08-194-087-15	Sequence 15, Appl
C 29	52.6	11.2	10596	5	PCT-US93-04648-15	Sequence 15, Appl
C 30	52.6	11.2	32207	2	US-08-770-379-20	Sequence 20, Appl
C 31	52.6	11.2	32207	4	US-08-757-669A-20	Sequence 20, Appl
C 32	52.6	11.2	32207	4	US-09-230-371A-20	Sequence 20, Appl
C 33	52	11.0	2790	2	US-08-718-661-1	Sequence 1, Appl
C 34	51.2	10.9	1518	2	US-08-820-170A-20	Sequence 20, Appl
C 35	51.2	10.9	1518	3	US-09-055-699-20	Sequence 20, Appl
C 36	51.2	10.9	1518	4	US-09-273-565-20	Sequence 20, Appl
C 37	51.2	10.9	1518	4	US-09-565-538-20	Sequence 20, Appl
C 38	51.2	10.9	2636	2	US-08-820-170A-21	Sequence 21, Appl
C 39	51.2	10.9	2636	3	US-09-055-699-21	Sequence 21, Appl
C 40	51.2	10.9	2636	4	US-09-273-565-21	Sequence 21, Appl
C 41	51.2	10.9	2636	4	US-09-565-538-21	Sequence 21, Appl
C 42	50.8	10.8	543	6	5273901-6	Patent No. 5273901
C 43	50	10.6	16442	3	US-08-781-891-208	Sequence 208, App
C 44	49.6	10.5	2369	4	US-08-910-925-2	Sequence 2, Appl
C 45	49.6	10.5	7218	1	US-08-232-463-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-247-155-41
; Sequence 41, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET 021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 41
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 68..337
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 68..124
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 10
; OTHER INFORMATION: seq LVLLGVSIPLVSA/QN
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 462..467
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 482..497
; US-09-247-155-41

Query Match 95.2%; Score 448.4; DB 4; Length 497;
Best Local Similarity 98.5%; Pred. No. 8.6e-126;
Matches 463; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 ctttgaagcattttgtctgtcttccttcaggtcaccaccatgaagttcttagc 60
|||||

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bb 22 cttlgaagcatttttgctgtgtctccctgagatcttcaggatccaccatgaagtcttttagc 81
QY 61 agtctgtgtactcttgggagtttccatcttcttctgtctctctgcccagaatccgacaacagc 120
Db 82 agtctgtgtactcttgggagtttccatcttcttctgtctctctgcccagaatccgacaacagc 141
QY 121 tcttccagctgacagatccagctactggtctctactgtatgaagccctgtgatctga 180
Db 142 tgtctcagctgacagatccagctactggtctctactgtatgaagccctgtgatctga 201
QY 181 aaccactgtctgtcaacaacttgagacactgtgctgtctctactaccactgaaccacccgtgc 240
Db 202 aaccactgtctgtcaacaacttgagacactgtgctgtctctactaccactgaaccacccgtgc 261
QY 241 tcttaccactgtctgtcaacaacttgagacactgtgctgtctctactaccactgaaccacccgtgc 300
Db 262 tcttaccactgtctgtcaacaacttgagacactgtgctgtctctactaccactgaaccacccgtgc 321
QY 301 lggtagagtgltccctgagatggaatccagcttctgagcttctgcaattgggtccacaacta 360
Db 322 lggtagagtgltccctgagatggaatccagcttctgagcttctgcaattgggtccacaacta 380
QY 361 ttcagctctctgtgatttccatccactacttacccttctgcttaccatccctttatctc 420
Db 381 ttcagctctctgtgatttccatccactacttacccttctgcttaccatccctttatctc 440
QY 421 tttacagttatttttttttttttttttttttttttttttttttttttttttttttttttt 470
Db 441 tttacagttatttttttttttttttttttttttttttttttttttttttttttttttttt 490

RESULT 2
US-09-253-691-3/c
: Sequence 3, Application US/09253691
: Patent No. 6124100
: GENERAL INFORMATION:
: APPLICANT: Dong Kyu JIN
: TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
: FILE REFERENCE: 1942/36
: CURRENT APPLICATION NUMBER: US/09/253,691
: CURRENT FILING DATE: 1999-02-22
: EARLIER FILING DATE: KR 98-6,278
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: WordPerfect 6.1/Windows
: SEQ ID NO 3
: LENGTH: 397
: TYPE: DNA
: ORGANISM: human
US-09-253-691-3

Query Match 14.6%; Score 68.6; DB 3; Length 397;
Best Local Similarity 61.5%; Pred. No. 1.9e-11;
Matches 110; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 75 tggaggttccactcttcttctgctcttccagaaatccgacaacagctgtccagctgaca 134
Db 397 TGCCCTTTCACATGGATGTGAACCTCTGTCTGATAGTCCCGCTGCTGTCTGCTGCTG 338
QY 135 cgtatccagctactggtctctgtatgaagccctctgagctgtgaaacacactgtctg 194
Db 337 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 278
QY 195 caacaactggacactgtgctcttaccactgtgcttaccactgaaccacgctgtttaccactgct 253
Db 277 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 219

RESULT 3
US-09-135-994-1/c
: Sequence 1, Application US/09135994A
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: Patent No. 6280938
: GENERAL INFORMATION:
: APPLICANT: Ranum et al.
: TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
: FILE REFERENCE: University of Minnesota
: CURRENT APPLICATION NUMBER: US/09/135,994A
: CURRENT FILING DATE: 1998-08-18
: EARLIER FILING DATE: 1997-08-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 477
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-135-994-1

Query Match 13.9%; Score 65.4; DB 4; Length 477;
Best Local Similarity 63.9%; Pred. No. 1.9e-10;
Matches 99; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 99 ctgcccagaatccgacaacagctgtccagctgacacgtatccagctactgtgctctgctc 158
Db 300 CTGCGGAGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
QY 159 atgatgaagccctgtgctgctgaaacacactgtctgcaacaactggacacactgtctc 218
Db 240 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
QY 219 ctaccactgcaaccacgctgtcttaccactgct 253
Db 180 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 146

RESULT 4
US-08-469-802B-3/c
: Sequence 3, Application US/08469802B
: Patent No. 5741645
: GENERAL INFORMATION:
: APPLICANT: Orr, Harry T.
: APPLICANT: Ranum, Laura P.W.
: APPLICANT: Chung, Ming-yi
: APPLICANT: Zoghbi, Huda Y.
: TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
: Patent No. 5741645
: TITLE OF INVENTION: Type 1 and Method for Diagnosis
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
: STREET: 119 No. 5741645th Fourth Street, Suite 203
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469,802B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Muetting, Ann M.
: REGISTRATION NUMBER: 33,977
: REFERENCE/DOCKET NUMBER: 110.00030101
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-305-1217
: TELEFAX: 612-305-1225
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-320-559-29

Query Match      13.8%; Score 64.8; DB 1; Length 3376;
Best Local Similarity 57.4%; Pred. No. 8.5e-10;
Matches 117; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 43 caccatgaagtcttagcagctcgggtactctctggaggtttccatcttcttctgctctgc 102
Db 844 CACTTTTATGTTCTCTCGAGCTCTTTAGAGGTTTTTCCCTTGCTGCTCCTTCAATTTGT 785

Qy 103 ccagaatccgacacagctgctccagctgacacgtatccagctactggtcctgctgatga 162
Db 784 GAGGCTTTGAAAACAGTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725

Qy 163 tgaagccctgagctgaaacacactctctgcaacaaactgacgacactgctgctctac 222
Db 724 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665

Qy 223 cactgcaacacacgctgctctctac 246
Db 664 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641

RESULT 7
US-08-545-860D-29/c
; Sequence 29, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6040140ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443

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; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-545-860D-29

Query Match      13.8%; Score 64.8; DB 3; Length 3376;
Best Local Similarity 57.4%; Pred. No. 8.5e-10;
Matches 117; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 43 caccatgaagtcttagcagctcgggtactctctggaggtttccatcttcttctgctctgc 102
Db 844 CACTTTTATGTTCTCTCGAGCTCTTTAGAGGTTTTTCCCTTGCTGCTCCTTCAATTTGT 785

Qy 103 ccagaatccgacacagctgctccagctgacacgtatccagctactggtcctgctgatga 162
Db 784 GAGGCTTTGAAAACAGTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725

Qy 163 tgaagccctgagctgaaacacactctctgcaacaaactgacgacactgctgctctac 222
Db 724 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665

Qy 223 cactgcaacacacgctgctctctac 246
Db 664 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641

RESULT 8
PCT-US94-04496-29/c
; Sequence 29, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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Query Match 13.7%; Score 64.6; DB 4; Length 203;
Best Local Similarity 59.6%; Pred. NO. 2.1e-10;
Matches 109; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Query Match	13.5%	Score 63.4;	DB 1;	Length 168;
Best Local Similarity	63.4%	Pred. NO. 4.4e-10;		
Matches 97; Conservative	0;	Mismatches 56;	Indels 0;	Gaps 0;


```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/267,803B
; FILING DATE: 28-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 110.00030120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-267-803B-5

Query Match 13.5%; Score 63.4; DB 2; Length 171;
Best Local Similarity 63.4%; Pred. No. 4.4e-10;
Matches 97; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 101 gccagaaatccgacacagctgtccagctgacacgtatccagctactgctgtgat 160
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 166 GCCCGGAGCCCTGCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107

QY 161 gatgaagccctgatgtgaaacacactgtctgtcgacaaactcgaccactgtctct 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 106 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 47

QY 221 accactgaacacacccgtctctaccactgt 253
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Db 46 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14

RESULT 14
US-08-469-802B-2/c
; Sequence 2, Application US/08469802B
; Patent No. 5741645
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5741645
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: 119 No. 5741645th Fourth Street, Suite 203
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,802B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00030101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1225
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-469-802B-2

Query Match 13.5%; Score 63.4; DB 1; Length 195;
Best Local Similarity 63.4%; Pred. No. 4.8e-10;
Matches 97; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 101 gccagaatccgacacacagctgtccagctgacacgtatccagctactgctgtgat 160
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 GCCCGGAGCCCTGCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131

QY 161 gatgaagccctgatgtgaaacacactgtctgtcgacaaactcgaccactgtctct 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 71

QY 221 accactgaacacacccgtctctaccactgt 253
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38

RESULT 15
US-08-267-903B-2/c
; Sequence 2, Application US/08267803B
; Patent No. 5834183
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/267,803B
; FILING DATE: 28-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 110.00030120
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12 ctttgaagcatttttctgtgtctccctgagatcttccaggtccaccacatgaagttcttagc 71
61 agtctgtgtactcttggagagttccatcttcttggtctctgcccagaatccgacaacagc 120
72 agtctgtgtactcttggagagttccatcttcttggtctctgcccagaatccgacaacagc 131
121 tgcctcagctgacacatctatccagctactggtctctgctgagatgaagcccttgatctga 180
132 tgcctcagctgacacatctatccagctactggtctctgctgagatgaagcccttgatctga 191
181 aaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccacccgtgc 240
192 aaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccacccgtgc 251
241 tctaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccacccgtgc 300
252 tctaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccacccgtgc 311
301 tggtagagtgctccctgagatgaatcagcttgagcttcttcaaatgggttgggagatcccgaa 360
312 tggtagagtgctccctgagatgaatcagcttgagcttcttcaaatgggttgggagatcccgaa 370
361 tctatgctctctgagtttcttcaactatcttaccctgctcagatatacccttttatctc 420
371 tctatgctctctgagtttcttcaactatcttaccctgctcagatatacccttttatctc 430
421 taatcagatttatttttcaataataaaaaaactatgagagcgtaacaa 470
431 taatcagatttatttttcaataataaaaaaactatgagagcgtaacaa 480

RESULT 6
AAX00644
ID AAX00644 standard; DNA; 489 BP.
AC AAX00644;
XX
XX
DT 25-MAR-1999 (first entry)
XX
DE Human secreted protein gene 34 clone HMQA164.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
PN W09842738-A1.
XX
PD 01-OCT-1998.
XX
PF 19-MAR-1998; 98WO-US05311.
XX
PR 30-MAY-1997; 97US-0050937.
PR 21-MAR-1997; 97US-0041276.
PR 21-MAR-1997; 97US-0041277.
PR 21-MAR-1997; 97US-0041281.
PR 21-MAR-1997; 97US-0042344.
PR 30-MAY-1997; 97US-0048069.
PR 30-MAY-1997; 97US-0048094.
PR 30-MAY-1997; 97US-0048095.
PR 30-MAY-1997; 97US-0048096.
PR 30-MAY-1997; 97US-0048099.
PR 30-MAY-1997; 97US-0048131.
PR 30-MAY-1997; 97US-0048135.
PR 30-MAY-1997; 97US-0048154.
PR 30-MAY-1997; 97US-0048160.
PR 30-MAY-1997; 97US-0048186.

PR 30-MAY-1997; 97US-0048187.
PR 30-MAY-1997; 97US-0048188.
PR 30-MAY-1997; 97US-0048350.
PR 30-MAY-1997; 97US-0048351.
PR 30-MAY-1997; 97US-0048352.
PR 30-MAY-1997; 97US-0048355.
PR 05-AUG-1997; 97US-0054804.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
PI Rosen CA, Ruben SM, Shi Y, Young P;
XX
DR WPI; 1999-070066/06.
P-PSDB; AAW67840.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 198; 385pp: English.
XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAX00602) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 87 novel genes and their fragments (nucleic
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 87
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAX00611 for described uses).
XX
SQ Sequence 489 BP; 125 A; 134 C; 87 G; 143 T; 0 other;

Query Match 95.2%; Score 448.4; DB 20; Length 489;
Best Local Similarity 98.5%; Pred. No. 2e-113;
Matches 463; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 ctttgaagcatttttctgtgtctccctgagatcttccaggtccaccacatgaagttcttagc 60
|||||
Db 9 ctttgaagcatttttctgtgtctccctgagatcttccaggtccaccacatgaagttcttagc 68

QY 61 agtctgtgtactcttggagagttccatcttcttggtctctgcccagaatccgacaacagc 120
|||||
Db 69 agtctgtgtactcttggagagttccatcttcttggtctctgcccagaatccgacaacagc 128

QY 121 tgcctcagctgacacatctatccagctactggtctctgctgagatgaagcccttgatctga 180
|||||
Db 129 tgcctcagctgacacatctatccagctactggtctctgctgagatgaagcccttgatctga 188

QY 181 aaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccacccgtgc 240
|||||
Db 189 aaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccacccgtgc 248

QY 241 tctaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccacccgtgc 300
|||||
Db 249 tctaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccacccgtgc 308

QY 301 tggtagagtgctccctgagatgaatcagcttgagcttcttcaaatgggttgggagatcccgaa 360
|||||
Db 309 tggtagagtgctccctgagatgaatcagcttgagcttcttcaaatgggttgggagatcccgaa 367

QY 361 tctatgctctctgagtttcttcaactatcttaccctgctcagatatacccttttatctc 420
|||||
Db 368 tctatgctctctgagtttcttcaactatcttaccctgctcagatatacccttttatctc 427

QY 421 taatcagttatttttcttccaaataaataaactatgagcgagtaaca 470
|||||
Db 428 taatcagttatttttcttccaaataaataaactatgagcaaaaaa 477

RESULT 7
AAZ40783
ID AAZ40783 standard; DNA; 497 BP.
XX AAZ40783;
XX
DT 18-JAN-2000 (first entry)
XX
DE Secreted protein EST coding sequence 108-002-5-0-F3-FL.
XX
KW Secreted protein; fingerprint identification technique;
KW chromosome mapping; human; hereditary disease; diagnosis; cancer;
KW hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy;
KW autoimmune disease; rheumatic disease; embryogenic disorder; myopathy;
KW renal injury; amino aciduria; hypoglycaemia; male rat infertility;
KW hypertension; ss.
XX
OS Homo sapiens.
XX
XX WO9940189-A2.
XX
PD 12-AUG-1999.
XX
PF 09-FEB-1999; 99WO-1B00282.
XX
PR 09-FEB-1998; 98US-0074121.
PR 13-APR-1998; 98US-0081563.
PR 10-AUG-1998; 98US-0096116.
PR 04-SEP-1998; 98US-0099273.
XX
XX (CEST) GENSET.
XX

PJ Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX WPI; 1999-600966/51.
DR P-PSDB; AAY59655.
XX
XX Extended cDNAs useful for expressing secreted proteins and to obtain
XX specific antibodies -
XX
XX Claim 1: Page 150; 244pp; English.
XX
XX This sequence encodes a human secreted protein of the invention. The
XX extended cDNAs (or genomic DNAs obtainable from them) may be used to
XX prepare PCR primers and probes. These are useful for forensic matching or
XX positive identification by DNA sequencing. They may also be used in
XX alternative fingerprint identification techniques. Antibodies against the
XX proteins encoded by the extended cDNAs are useful in identification of
XX tissue types or cell species, as well as identifying tissue specific
XX soluble proteins. The sequences can be used for chromosome mapping and
XX identification of genes associated with hereditary diseases or drug
XX response. Signal sequences from the cDNAs can be used in construction of
XX secretion vectors. Other sequences derived from the extended cDNAs can be
XX used to clone upstream genomic DNA sequences including promoters. This is
XX in turn useful for identifying proteins that interact with promoter
XX sequences. Some of the proteins may be useful in diagnosing and treating
XX several disorders including, but not limited to: cancer, hyperlipidaemia,
XX cardiovascular and neurodegenerative disorders, autoimmune diseases, and
XX rheumatic diseases, embryogenic disorders, hypertension, renal injury,
XX amino acidurias, hypoglycaemia, male rat infertility and myopathies.
XX
XX Sequence 497 BP; 122 A; 138 C; 90 G; 147 T; 0 other;

Query Match 95.2%; Score 448.4; DB 20; Length 497;
Best Local Similarity 98.5%; Pred. No. 2e-113;
Matches 463; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 ctttgaagcatttttctgtctccctgatctctcaggtccaccacatgaagttcttlayc 60
|||||
Db 22 ctttgaagcatttttctgtctccctgatctctcaggtccaccacatgaagttcttlayc 81
QY 61 agtctctgttactcttgggagtttccatcttcttggctctgccagaatccgacaacagc 120
|||||
Db 82 agtctctgttactcttgggagtttccatcttcttggctctgccagaatccgacaacagc 141
QY 121 tgctccagctgacagctatccagctactgtctctgtctgatgatgaagccctgatgctga 180
|||||
Db 142 tgctccagctgacagctatccagctactgtctctgtctgatgatgaagccctgatgctga 201
QY 181 aacctgtctgtgcaacaactgcgacctgtctcttaccactgcaaccaccgctgc 240
|||||
Db 202 aacctgtctgtgcaacaactgcgacctgtctcttaccactgcaaccaccgctgc 261
QY 241 ttctaccactgtctgtaaaagacattccagttttaccacaaatgggtgggattctcccgaa 300
|||||
Db 262 ttctaccactgtctgtaaaagacattccagttttaccacaaatgggtgggattctcccgaa 321
QY 301 tggtagagtgtccctgagatggaatcagcttgagctcttctgcaattgggtgcacaacta 360
|||||
Db 322 tggtagagtgtccctgagatggaatcagcttgagctcttctgcaattgggtgcacaacta 380
QY 361 ttcatgtctctgtgatttccatccaaactacttacccttgctacgataccccctttatctc 420
|||||
Db 381 ttcatgtctctgtgatttccatccaaactacttacccttgctacgataccccctttatctc 440
QY 421 taatcagttatttttcttccaaataaaaaataactatgagcgagctaaaca 470
|||||
Db 441 taatcagttatttttcttccaaataaaaaataactatgagcaaaaaaaa 490

RESULT 8
AAC79470
ID AAC79470 standard; cDNA; 578 BP.
XX
AC AAC79470;
XX
DT 07-FEB-2001 (first entry)
XX
XX cDNA sequence of human breast tumour clone B511S.
DE Human; breast tumour antigen; cytostatic; immunotherapy;
KW breast cancer; vaccine; ss.
XX
XX Homo sapiens.
XX
XX WO200061756-A2.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US09688.
XX
PR 09-APR-1999; 99US-0288950.
PR 02-JUL-1999; 99US-0346327.
XX
XX (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J, Dillon DC;
XX
XX WPI; 2000-638568/61.
DR
XX P-PSDB; AAB28525.
XX
PT A novel isolated polypeptide comprising an immunogenic portion of a
PT breast cancer protein useful in the detection and treatment of breast
PT cancer -
XX
XX Claim 4; Page 88; 95pp; English.

XX
XX The present sequence was isolated from a breast tumour cDNA library. It
CC is provided in a specification relating to compounds for immunotherapy

PF 28-FEB-2001; 2001WO-US06516.
 XX
 PR 29-FEB-2000; 2000US-0516444.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
 PI Russell JC, Stroupe SD;
 XX
 DK MPI; 2001-596773/67.
 XX
 XX A gene or its fragment which codes for a BS106 polypeptide, useful for
 PT the detection of a breast disease such as breast cancer -
 XX
 PS Example 1; Fig 1; 158pp; English.
 XX
 CC The invention relates to human BS106-specific polypeptides and
 CC polynucleotides. The BS106 polypeptides and antibodies are useful
 CC for detecting, diagnosing, staging, monitoring, prognosticating,
 CC preventing, treating or determining the predisposition of an
 CC individual to diseases and conditions of the breast such as breast
 CC cancer. They are also useful in the treatment of tumours or
 CC metastases. Polynucleotides of the invention are useful in drug
 CC screening and gene therapy. The present sequence is human BS106
 CC gene specific full length cDNA, expressed sequence tag (EST) clone
 CC 1662885inh.
 XX
 SQ Sequence 472 BP; 108 A; 134 C; 86 G; 144 T; 0 other;

Query Match 94.7%; Score 446.2; DB 22; Length 472;
 Rust Local Similarity 99.1%; Pred. No. 8e-113;
 Matches 459; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 ctttgaagcaattttgtctgtcctcctgatcttcaggctcaccacatgaagtctctagc 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 9 ctttgaagcaattttgtctgtcctcctgatcttcaggctcaccacatgaagtctctagc 68
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 61 agtctcgtgactcttggggagttccatctttctgtctgtcccaaatccgacacagc 120
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 69 agtctcgtgactcttggggagttccatctttctgtctgtcccaaatccgacacagc 128
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 121 tgcctcagctgacacgtatccagctactgctcctctgatgatgaagccctgatgctga 180
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 129 tgcctcagctgacacgtatccagctactgctcctctgatgatgaagccctgatgctga 188
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 181 aaccactgctgctgaacactgcgaccactgctcctctaccactgcaaccacgcctgc 240
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 189 aaccactgctgctgaacactgcgaccactgctcctctaccactgcaaccacgcctgc 248
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 241 ttctaccactgctcgttaagagacattccagttttaccacaaatgggtggggtctcccgaa 300
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 249 ttctaccactgctcgtlaagagacattccagttttaccacaaatgggtggggtctcccgaa 308
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 301 tggtagagtggtccctgagatggaatcagcttgagttcttgcgaattgggtgcacaaacta 360
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 309 tggtagagtggtccctgagatggaatcagcttgagttcttgcgaatt-ggtcacaaacta 367
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 361 ttcatgcttccctggtgatcttcacactacttaccttgctcactgatatcccttttatctc 420
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 368 ttcatgcttccctggtgatcttcacactacttaccttgctcactgatatcccttttatctc 427
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 421 taatcagttttatttttttcaataaaaaataactatgagcga 463
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 428 taatcagttttatttttttcaataaaaaataactatgagcga 470
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 04:00:45 ; Search time 1900.29 Seconds
(Without alignments)
5186.787 Million cell updates/sec

Title: US-09-525-361A-23

Perfect score: 471
Sequence: 1 cttgaagcatttcgtctg.....aactatgagcgagctaacat 471

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl:*
- 1: gb_ba:*
 - 2: gb_htg:*
 - 3: gb_in:*
 - 4: gb_om:*
 - 5: gb_ov:*
 - 6: gb_pat:*
 - 7: gb_ph:*
 - 8: gb_pl:*
 - 9: gb_pr:*
 - 10: gb_ro:*
 - 11: gb_srs:*
 - 12: gb_sy:*
 - 13: gb_un:*
 - 14: gb_vl:*
 - 15: em_ba:*
 - 16: em_fun:*
 - 17: em_hum:*
 - 18: em_in:*
 - 19: em_mu:*
 - 20: em_om:*
 - 21: em_or:*
 - 22: em_ov:*
 - 23: em_pat:*
 - 24: em_ph:*
 - 25: em_pl:*
 - 26: em_to:*
 - 27: em_sts:*
 - 28: em_un:*
 - 29: em_vl:*
 - 30: em_htg_hum:*
 - 31: em_htg_inv:*
 - 32: em_htg_other:*
 - 33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

1	448.4	95.2	497	6	AR177347	Sequence	AR177347
2	448.4	95.2	578	6	AX282981	Sequence	AX282981
3	447	94.9	482	6	BD007431	Reagent a	BD007431
4	446.8	94.9	553	6	BD007432	Reagent a	BD007432
5	446.2	94.7	472	6	AX240679	Sequence	AX240679
6	446.2	94.7	473	6	AX240680	Sequence	AX240680
7	445.4	94.6	472	6	AX328498	Sequence	AX328498
8	442.2	93.9	488	6	AX067322	Sequence	AX067322
9	383.4	81.4	396	9	AF141087	Homo sapi	AF141087
10	300.8	63.9	308	6	AX240676	Sequence	AX240676
11	300.8	63.9	308	6	BD007429	Sequence	BD007429
12	286.8	60.9	292	6	AX240677	Reagent a	AX240677
13	269.8	57.3	273	6	AX328499	Sequence	AX328499
14	255.6	54.3	264	6	AX079476	Sequence	AX079476
15	255.6	54.3	266	6	AX079475	Sequence	AX079475
16	247.2	52.5	291	6	AX079474	Sequence	AX079474
17	202.8	43.1	229	6	BD007428	Sequence	BD007428
18	187	39.7	133000	2	AC079842	Homo sapi	AC079842
19	187	39.7	188873	2	AC019223	Homo sapi	AC019223
20	187	39.7	222877	2	AC024091	Homo sapi	AC024091
21	186.4	39.6	201	6	AX240675	Sequence	AX240675
22	181.4	38.5	197	6	AX240678	Sequence	AX240678
23	181.4	38.5	197	6	BD007430	Sequence	BD007430
24	80.8	17.2	469	10	RATSP071	Reagent a	M33976 Rat salivary
25	70.2	14.9	397	6	BD010479	Diagnostic	BD010479 Diagnostic
26	69.6	14.8	1591	10	RNO6295	Mus muscu	AJ006295 Mus muscu
27	69.6	14.8	68409	2	AC105975	Mus muscu	AC105975 Mus muscu
28	69.6	14.8	185363	2	AC094466	Mus muscu	AC094466 Mus muscu
29	69.4	14.7	5727	2	AY045719	Mus muscu	AY045719 Mus muscu
30	68.8	14.6	666	8	AF413050S2	Larus aud	AF413051 Zea mays
31	68.8	14.6	46904	2	AC100911	Mus muscu	AC100911 Mus muscu
32	67.8	14.4	98221	2	AC097839	Rattus no	AC097839 Rattus no
33	67.6	14.4	155780	9	HS336012	Homo sapi	AL513498 Homo sapi
34	67.6	14.4	175695	2	AL606844	Homo sapi	AL606844 Homo sapi
35	67.2	14.3	180668	2	AC020857	Mus muscu	AC020857 Mus muscu
C 36	66.8	14.2	110000	2	AC092202_1	Continuation (2 of	AC092203 Mus muscu
C 37	66.8	14.2	173851	2	AC096966	Rattus no	AC096966 Rattus no
C 38	66.8	14.2	204152	2	AC092203	Mus muscu	AY057052 Mamestra
39	66.6	14.1	2960	3	AF139019	Cepaea ne	AF139019 Cepaea ne
40	66.4	14.1	624	3	AF139019	Cepaea ne	AF139019 Cepaea ne
41	66.4	14.1	236962	2	AL606742	Mus muscu	AL606742 Mus muscu
42	66.2	14.1	223398	5	FR0271723	Fugu rubr	AJ2271723 Fugu rubr
C 43	66.2	14.1	229380	2	AC079636	Mus muscu	AF051726 Mus muscu
44	66	14.0	5719	10	MMCATSI	Cosmid c1	AC002053 Cosmid c1
45	66	14.0	27613	9	AC002053	Cosmid c1	

ALIGNMENTS

RESULT 1

AR177347 LOCUS AR177347 497 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 41 from patent US 6312922.

ACCESSION AR177347

VERSION AR177347.1 GI:17919702

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 497)

AUTHORS Edwards,J.-R.,Dumas,Milne., Duclert,A. and Bouguetelert,I..

TITLE Complementary DNAs

JOURNAL Patent: US 6312922-A 41 06-NOV-2001;

FEATURES

source Location/Qualifiers

1..497 /organism="unknown"

BASE COUNT 122 a 138 c 90 g 147 t

ORIGIN

Query Match 95.2% Score 448.4; DB 6; Length 497;
Best Local Similarity 98.5% Pred. No. 1.6e-96;

OY	121	tgctccagctgacacgtaaccagctacacgctcgtcgtatgataagaaagccctgacgtcga	180
	111		
Db	137	tgctccagctgacacggtatccagctactgctcgtctctatgataaagccctgactgta	196
	111		
OY	181	aaccactgctgctgcacaacaactcgtgacaactcgtcctccctaccactgcaaccacccgtgc	240
	111		
Db	197	aaccactgctgctgcgaaccacactgcacacactgctcgtctctaccactgcgaaccacccgtgc	256
	111		
OY	241	ttctccacactgctgtaagagacatccggtttaccaccaatgggtgtgggaactcccgaa	300
	111		
Db	257	ttctccacactgctgctgaataagacattccacagttttaccaccaatgggtgggacattcccgaa	316
	111		
OY	301	tggtagagatgctccctgagatcggaacacagctctgagctctcgcgaattgggtcacacaacta	360
	111		
Db	317	tggtagagagtgctccctgagatcggaatcagctctgagctctcgcgaattgggtcacacaacta	375
	111		
OY	361	ttcacatgctcctgatalttcatcacaactactaacctctgcctcagaataaccctctatcctc	420
	111		
Db	376	ttcacatgctcctgataatttcacccaactgctgagctctcgcgaattgggtcacacaacta	445
	111		
OY	421	taatacagttatattctctctcaaaaataaatacctacagacgaactaaca	470
	111		
Db	436	taatacagttatattctctctcaaaaataaatacctacagacgaactaaca	485
	111		

RESULT	3
LOCUS	BD007431
DEFINITION	BD007431 482 bp DNA linear PAT 31-JAN-2002
ACCESSION	Reagent and method useful in detecting mammary diseases.
VERSION	BD007431.1 GI:18635802
KEYWORDS	JP 2001503980-A/4.
SOURCE	unidentified.
ORGANISM	unclassified.
AUTHORS	1 (bases 1 to 482) Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvill,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D. Reagent and method useful in detecting mammary diseases Patent: JP 2001503980-A 4 27-MAR-2001; ABBOTT LABORATORIES
TITLE	OS Unidentified
JOURNAL	PN JP 2001503980-A/4
COMMENT	PD 31-MAR-2001 PF 31-OCT-1997 JP 1998520795 PR 31-OCT-1996 US 08/742067 PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACY L COLPITTS, PI POLA N FRIEDMAN, PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, PI MICHAEL R KLASS, PI JOHN D KRATOCHVILL, LISA ROBERTS RAPP, JOHN C RUSSELL, PI STEVEN D STROUPE PC C12N15/09,A61K38/00,A61K39/395,A61P35/00,C07K14/47, PC C07K16/30, PC C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12M15/00,C12M5/00, PC A61K37/02 CC Strandedness: Single; CG Topology: Linear; FH key location/unalifiers FT source 1..482 /organism='Unidentified'. FT location/unalifiers 1..482 /organism='unidentified' /db_xref='taxon:32644'
BASE COUNT	109 a 136 c 90 g 145 t 2 others
ORIGIN	
Query Match	94.9%: Score 447; DB 6; Length 482;
Best Local Similarity	98.9%: Pred. No. 3,5e+96;
Matches 458: Conservative	2: Mismatches 1: Indels 1: gaps 1:

FEATURES	source
1	ctttgaagcatttttgctcgtgctcccgatcttaagtcacaccagaagtcttcgac 60
18	ctttgaagcatttttgctcgtgctcccgatcttaagtcacaccagaagtcttcgac 77
OY	61 agctcgtgtaactcttgaggagttccatctcttcgtctcctgcagaatccgacaagc 120
Db	78 AGCTCTGGTACTCTTGAGGAGTTCCATCTTTTCTGGTCTCTGCCGAATCCGACAAACGC 137
OY	121 tgcctcaagctgacacgataccagctactgctcgtcgtatgatagaagccctgactgta 180
Db	138 TGCTCCACACTGCACGATATCCAGCTACTAGTGTCTCTGTATGAAGCCCTGATGTCTGA 197
OY	181 aaccctctgctgtgtaaacacactgagcaaccactgctcctcctaccactgtaaacaccgctgc 240
Db	198 AACCACTCTCTGTGGAAACCACTGCACCACTGCTCTCTTACCACTGCACCAACCGCTGC 257
OY	241 ttctccacactgctgtaagaacatccagatttaccaaatggtgtggagatctccgaa 300
Db	258 TTCTACCACTGCTGCTTAAGAATTCAGATTTTACCCAATGGTGGGAGATCTTCGGA 317
OY	301 tggtagagtggtgctccctgagagatgaaacagcttgagctgctctgcaattggtgtaacaacta 360
Db	318 TGGTAGAGTGTGTCTCCCTGAGATGAGTAAGCTGTGAGCTTCTTGCAATT -GGTCACACACTA 376
OY	361 ttcaagctcctcgtgatttcaatccaactactactgctcctcgtacgatatcccttatctc 420
Db	377 TTCAAGCTTCTCGTGATTTTCATCCACAGTACTTACCTTCCCTACGATATCCCTTTATCTGC 436
OY	421 taatcagcttaattctcttccaataaataaataaactatgagca 463
Db	437 TAATCAGTTTATTTCTTTCAATATAAATAATACATATGACGA 479
RESULT 4	
LOCUS	BD007432 553 bp DNA linear PAT 31-JAN-2002
DEFINITION	Reagent and method useful in detecting mammary diseases.
ACCESSION	BD007432
VERSION	BD007432.1 GI:18635803
KEYWORDS	JP 2001503980-A/5.
SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	1 (bases 1 to 553)
AUTHORS	Medel,P.A.B., Cohen,M., Colpits,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D. Reagent and method useful in detecting mammary diseases Patent: JP 2001503980-A 5 27-MAR-2001;
TITLE	ABROTT LABORATORIES
JOURNAL	OS Unidentified
COMMENT	PN JP 2001503980-A/5 PD 27-MAR-2001 PR 31-OCT-1997 JP 1998520795 PF 31-OCT-1996 US 08/742067 PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACY L COLPITTS, PI POLA N FRIEDMAN, PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES, PI MICHAEL R KLASS, PI JOHN D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL, PI STEVEN D STROUPE. PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P35/00,C07K14/47, PC C07K16/30, PC C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00, PC A61K37/02 CC Strandedness: Single; CC Topology: Linear; CC FH key FT source FT 1..553 Location/Qualifiers 1..553 /organism='unidentified'.

BASE COUNT	159 a	144 c	101 g	148 t	1 others
ORIGIN	/organism="unidentified" /db_xref="taxon:32644"				
Query Match	94.9%	Score 446.8	DB 6	Length 553	
Best Local Similarity	98.3%	Pred. No. 3.9e-96			
Matches 462	Conservative	0	Mismatches 7	Indels 1	Gaps 1
OY	1	cttgaagcattttgtcgtcgtccccaatctcaagtcaccacagaagtcttcaac	60		
DB	32	CTTTGACAGATTTTTGTCTGTCTCTCCCTATCTTCAATGTCACACACATGAATTTCTTACC	91		
OY	61	agtcctgtgtactcttgggaatttccatcttcttggctctcgtccagaatcgcacaacac	120		
DB	92	ACTCTGTGACTCTTGGGAGATTTCATCTTCTGTGCTGTGCCAGAAATCGACAAACGC	151		
OY	121	tgtctgaagtcgaagataccagcctacgtgtcttcgtctgaatgttgaagccctcgatctga	180		
DB	152	TGCTTCAGCTGACAGCTATACGCTACGTGTCTCTCTGTATGAAGCCCTGTATGCTTCA	211		
OY	181	aaccacgtcgtcgtcaacaacgtgcagccactgtctgtcttaccactgcaaacaccgtctac	240		
DB	212	AACCACTGCTGCTGCACACACACCTGCCACCTCTGCTCTTACCACTGCACACACCGCTGC	271		
OY	241	ttctaacacgtcgtcgtlaaagacatctccagtttaccccaatgtgttgggaatctccgaa	400		
DB	272	TTCCTACCACTGCTCTGTAAGACATTCCTCAATTTTACCCAAATGGTGTGGGATCTCCGAA	331		
OY	301	tgttgagatgtgtccctgtgaagatgaatcaacttgaatctcttcgcaatttngtccaaac	360		
DB	332	TGGTAGAGTGTCTCCCTGATGATGATACGCTGTGAGTCTTGCATTT-GGTCACAACTTA	390		
OY	361	ttcatgtcttctgtatatttcatccaaacttacttaccttgaagatcagatctcccttattctc	420		
DB	391	TTCATGCTTCCGCTGATTTATTCATCCAACTACTTACTCTGCTACGATATGCCCTTTATCTGC	450		
OY	421	taatcagtttattcttcttcaataaaataaactatagacagactaaca	470		
DB	451	TAACTAGTTTATTTCTTTCAATTAATAAATTAACATATGACAAACAATAA	500		
RESULT 5					
AX240679	LOCUS	AX240679	472 bp	DNA	linear
DEFINITION	Sequence 5 from Patent WO0165262.				
ACCESSION	AX240679				
VERSION	AX240679.1	GI:15797662			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
	1 (bases 1 to 472)				
TITLE	Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,				
JOURNAL	Roberts-Rapp, L., Russell, J.C., Hodges, S.C., Kias, M.R., Kratochvil, J.D.,				
	Reagents and methods useful for detecting diseases of the breast				
	Patent: WO 0165262-A 5 07-SEP-2001;				
FEATURES	ABBOY LABORATORIES (US)				
source	Location/Qualifiers				
	1..472				
BASE COUNT	/organism="Homo sapiens"				
ORIGIN	/db_xref="taxon:9606"				
	108 a	134 c	86 g	144 t	
Query Match	94.7%	Score 446.2	DB 6	Length 472	
Best Local Similarity	99.1%	Pred. No. 5.4e-96			
Matches 459	Conservative	0	Mismatches 3	Indels 1	Gaps 1

OY 1 cttgaagcattttgtctgtgtccctgaltcctcaagtcacacatgaagttcttagc 60
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DB 9 CTTTGAAGCATTTTTGTCTGTGCTCCTGATCTTCATGTACACACATGAAAGTTCTTAGC 68
OY 61 agtctgtactcttgggaatttccatcttctgtgtctgtccccaagaatccgacaaagc 120
|||||
DB 69 AGTCTGTACTCTTGGGAGTTTCCATCTTGTGCTGTGCCAGAAATCCGCAACAGC 128
OY 121 tgcctcagctgacacagatcctcaagctactgtgtccctgtatgataagaaacccctatgtcga 180
|||||
DB 129 TGCTCCAGCTGACACGATATCCAGTACTGCTCCTGATGATGAACCCCTGATGCTGA 188
OY 181 aacacgtctgtctgacaaactgcagcactgtgtctctaccatctgcaacacccgtctgc 240
|||||
DB 189 AACCACTGCTGTGCAACCACTGCGACACTGCTGCTCCACCACTGCAACCAACCGCTGC 248
OY 241 tttccacactgtctgtgaagaacatcctcaagtttccacaaatgggttgggaatctccgaa 300
|||||
DB 249 TTCTACCACTGCTGCTGAAGACATTCACATTTTACCCAAATGGGTTGGGATGTCGCCGA 308
OY 301 tggtagaagtggtccctgagaatgaaatcagcttgaagctctgtcaatttgggtcacaaacta 360
|||||
DB 309 TGCTAGAGTGTGCTCCTGAGATGGAATCAGCTTGAGTCTTCTGCAAT- GGTCAACAATA 367
OY 361 tttcagttctcgtgtatcttccaaactacttactgtgtctgaagatacccttattctc 420
|||||
DB 368 TTGATGCTTCTGTGATTTATCCAACTTACTGCTGCTGAGATATCCCTTTATCTC 427
OY 421 taatcagttatttcttccaataaataactatgaagcga 463
|||||
DB 428 TAATCAGTTTATTCTTCTTCAATAAATAACTATGAGCAA 470

RESULT 6
LOCUS AX240680 473 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 6 from Patent WO0165262.
ACCESSION AX240680
VERSION AX240680.1 GI:15797663
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Billing-Medel,P.A., Cohen,M., Colplitis,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C. and Stroupe,S.D.
Reagents and methods useful for detecting diseases of the breast
TITLE Patent: WO 0165262-A 6 07-SEP-2001;
JOURNAL ABBOTT LABORATORIES (US)
FEATURES
source Location/Qualifiers
1..473
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 108 a 134 c 86 g 145 t
ORIGIN

Query Match 94.7%; Score 446.2; DB 6; Length 473;
Best Local Similarity 99.1%; Pred. No. 5.4e-96;
Matches 459; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
OY 1 cttgaagcattttgtctgtgtccctgaltcctcaagtcacacatgaagttcttagc 60
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DB 9 CTTTGAAGCATTTTTGTCTGTGCTCCTGATCTTCATGTACACACATGAAAGTTCTTAGC 68
OY 61 agtctgtactcttgggaatttccatcttctgtgtctgtccccaagaatccgacaaagc 120
|||||
DB 69 AGTCTGTACTCTTGGGAGTTTCCATCTTGTGCTGTGCCAGAAATCCGCAACAGC 128
OY 121 tgcctcagctgacacagatcctcaagctactgtgtccctgtatgataagaaacccctatgtcga 180
|||||

DB 129 TGCTCCAGCTGACACGATATCCAGTACTGCTGCTGCTGATGATGAAGCCCTGATGCTTGA 188
OY 181 aacacgtctgtctgacaaactgcagcactgtgtctctaccatctgcaacacccgtctgc 240
|||||
DB 189 AACCACTGCTGTGCAACCACTGCGACACTGCTGCTCCACCACTGCAACCAACCGCTGC 248
OY 241 tttccacactgtctgtgaagaacatcctcaagtttccacaaatgggttgggaatctccgaa 300
|||||
DB 249 TTCTACCACTGCTGCTGAAGACATTCACATTTTACCCAAATGGGTTGGGATGTCGCCGA 308
OY 301 tggtagaagtggtccctgagaatgaaatcagcttgaagctctgtcaatttgggtcacaaacta 360
|||||
DB 309 TGCTAGAGTGTGCTCCTGAGATGGAATCAGCTTGAGTCTTCTGCAAT- GGTCAACAATA 367
OY 361 tttcagttctcgtgtatcttccaaactacttactgtgtctgaagatacccttattctc 420
|||||
DB 368 TTGATGCTTCTGTGATTTATCCAACTTACTGCTGCTGAGATATCCCTTTATCTC 427
OY 421 taatcagttatttcttccaataaataactatgaagcga 463
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DB 428 TAATCAGTTTATTCTTCTTCAATAAATAACTATGAGCAA 470

RESULT 7
LOCUS AX328498 472 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0135811.
ACCESSION AX328498
VERSION AX328498.1 GI:18098424
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Mack,D. and Gish,K.C.
TITLE Novel methods of diagnosing and determining prognosis of breast
cancer, compositions, and methods of screening for breast cancer
modulators
JOURNAL Patent: WO 0135811-A 1 25-JAN-2001;
EOS Biotechnology, Inc. (US)
FEATURES
source Location/Qualifiers
1..472
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 109 a 132 c 88 g 143 t
ORIGIN

Query Match 94.6%; Score 445.4; DB 6; Length 472;
Best Local Similarity 99.2%; Pred. No. 8.4e-96;
Matches 469; Conservative 0; Mismatches 1; Indels 2;
OY 1 cttgaagcattttgtctgtgtccctgaltcctcaagtcacacatgaagttcttagc 60
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DB 1 CTTTGAAGCATTTTTGTCTGTGCTCCTGATCTTCAGCTGACACCAATGAAGTTCTTAGC 60
OY 61 agtctgtg--taactctggagatccatcttctgtgtctgtccccaagaatccgacaa 118
|||||
DB 61 AGCTCGATATCTGTGGAGATTTTCATCTTGTGCTGTGCCAGAAAT-CGACAA 119
OY 119 gctgtcagctgacacagatcctcaagctactgtgtcctgtatgataagcccttagcgt 178
|||||
DB 120 GCTGCTCCAGCTGACACGATATCCAGTACTGCTGCTGATGATGAAGCCCTGATGCT 179
OY 179 gaaacacagctgtgacaaactgcagcactgtgtcctccacacagcgaacacccct 218
|||||
DB 180 GAAACCACTGCTGTGCAACCACTGCGACCACTGCTGCTTACCACTGCAACCGCT 219
OY 239 gctctaccacagctcgttaaaagacatcccaaglllaaccnaaagqatlggaatcttcc 298
|||||
DB 240 GCTTACACACTGCTGCTGAAGACATTCAGTCTTACCCAAATGGGTTGGGATGTCGCC 299
|||||

LOCUS	AX067322	488 bp	DNA	Linear	PAT 24-JAN-2001
DEFINITION	Sequence	26 from Patent WO0078960.			
ACCESSION	AX067322				
VERSION	AX067322.1	GI:12544946			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Yuglu,J. and Mitcham,J.L.				
TITLE	Compositions and methods for the therapy and diagnosis of breast cancer				
JOURNAL	Patent: WO 0078960-A 26 28-DEC-2000;				
FEATURES	CORIXA CORPORATION (US)				
source	Location/Qualifiers				
	1..488				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	135 a 129 c 84 g 138 t				2 others
ORIGIN					
Query Match	93.9%	Score 442.2	DB 6	Length 488	
Best Local Similarity	98.3%	Pred. NO. 4.9e-95			
Matches	455; Conservative	2; Mismatches	5; Indels	1; Gaps	1;
Oy	8	gcaatttgctgctgctccctgatacttcaagtcacacccaagaagttctttagagctctg	67		
Db	1	GCATTTTGCTGCTCTCCCTGATTTTGAAGGCACACCATGAAAGTTCTTGACATCTCTG	60		
Oy	68	gtaaccttgagagtttccatcttctgctctctgcccagaalccgaacaagctgtctca	127		
Db	61	GTACCTTGGGAGTTTCCATCTTTTGGTCTCTGCCCAAGATCCGACACACGCTCTTCA	120		
Oy	128	gctgaacgataccagctactgctcgtctgatagtgaagccctgactgctgaaccact	187		
Db	121	GCTGACAGTATCCAGCTACTGCTCTCTGATGATGAAGCCCTGATGTGAACCACT	180		
Oy	188	gctgctgaacaacatgagacacgtctgctctctactaccatgtgaacacacgcgtctctac	247		
Db	181	GCTGTCGACACACCTGCCACCACTCTCTCTTACCACTGACACACCGCTTCTTACC	240		
Oy	248	actgctcgtlaaagacatccagtttaccacaatggtttgagatctccgaatggtaga	307		
Db	241	ACTGCTCTGTAAGACATTTCCAGTTTACCACCAATGGTTGGGAGATCTCCGATGTGTA	300		
Oy	308	gtgtgtccctgaagagatacagcttgagcttcttgcgaatctgggtcaacactatctatgc	367		
Db	301	GTGTGTCCCTGAGATGAGATCAGCTTGAGTCTTGTGCAATT-GGTGACACACTATTTCATGC	359		
Oy	368	tctcgtgatacttcaacactactactctgctcgaatctatcccttatcttcaatag	427		
Db	360	TTCCGTGATTTTCATCAACCAACTACTTACTTGCTGCTATGATATCCCTTTATCTATACG	419		
Oy	428	tttatcttcttcaaaataaaataactatgagcgagctaaaca	470		
Db	420	TTTTATTTTTTTCAAAATAAAATAACTATGACCAACTAAAA	462		

[illegible]

OY 361 ttcatgcttcctggtgattcccaactactacc 397
 Db 360 TTCAATGCTTCTGTGATTTCACTCACTTACCTT 396

RESULT 10

AX240676 308 bp DNA linear PAT 26-SEP-2001
 LOCUS AX240676
 DEFINITION Sequence 2 from Patent WO0165262.
 ACCESSION AX240676
 VERSION AX240676.1 GI:15797659
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 308)
 Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C., and Stroupe, S.D.
 Reagents and methods useful for detecting diseases of the breast

TITLE Patent: WO 0165262-A 2 07-SEP-2001;
 JOURNAL ABBOTT LABORATORIES (US)

FEATURES
 source Location/Qualifiers

1..308

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 63 a 94 c 65 g 86 t

ORIGIN

Query Match

63.9%; Score 300.8; DB 6; Length 308;

Best Local Similarity 99.3%; Pred. No. 2.2e-61;
 Matches 302; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctctgaagcattttgtctgctgctcctgagcttcaggtccaccacatgaagttcttagc 60
 Db 5 CTTTGAAGCATTTTGTCTGTCTGCTCCCTGATCTTCAGGTACCACTGAGTTCTTAGC 64
 OY 61 agtccgtgactccttgggaattccactcttctgctcctgcccagaatccgaacaagc 120
 Db 65 AGTCTGTGACTCTTGGAGTTTCATCTTGTGCTCTGCCAGAAATCGCAACAGC 124
 OY 121 tgcctcagctgcaacgatacctgactgctcctgctgctgatagaagaagccctgaatgctga 180
 Db 125 TGTCTCAGCTGACAGTATCAGTACTGTCTGCTGATGATGAACCCCTGATGCTGA 184
 OY 181 aaccactgctgctgcaacaactggaacactgctgctcctcaccactggaacacacgctgc 240
 Db 185 AACCACTGCTGCTGCAACCACTGCGACCACTGCTGCTCTTACCACTGCAACCGCTGC 244
 OY 241 ttctaccactgctgctgaagaacatltccagtttaccccaatgggttgggagatcccgaa 300
 Db 245 TTCTACCACTGCTGCTGAAGACATTCAGTTTACCCAAATGGGTTGGGATCTTCCGAA 304
 OY 301 tggc 304
 Db 305 TGGT 308

RESULT 11

BD007429

LOCUS BD007429 308 bp DNA linear PAT 31-JAN-2002
 DEFINITION Reagent and method useful in detecting mammary diseases.
 ACCESSION BD007429
 VERSION BD007429.1 GI:18635800
 KEYWORDS JP 2001503980-A/2.
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE
 1 (bases 1 to 308)
 Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,

Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C., and Stroupe, S.D.
 Reagent and method useful in detecting mammary diseases
 Patent: JP 2001503980-A 2 27-MAR-2001;
 JOURNAL ABBOTT LABORATORIES

COMMENT

OS Unidentified
 PN JP 2001503980-A/2
 PD 27-MAR-2001
 PF 31-OCT-1997 JP 1998520795
 PR 31-OCT-1996 US 08/742067
 PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACY L COLPITTS, PI
 POLA N FRIEDMAN,
 PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, PI MICHAEL
 R KLAS,
 PI JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, PI
 STEVEN D STROUPE
 PC C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P35/00,C07K14/47,
 PC C07K16/30,
 PC C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00, PC
 A61K37/02
 CC Strandedness: Single;
 CC Topology: Linear;
 FH key
 FT source Location/Qualifiers
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 /organism="Unidentified"
 /db_xref="taxon:32644"

BASE COUNT 63 a 94 c 65 g 86 t

ORIGIN

Query Match

63.9%; Score 300.8; DB 6; Length 308;

Best Local Similarity 99.3%; Pred. No. 2.2e-61;
 Matches 302; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctctgaagcattttgtctgctcctcctgagcttcaggtccaccacatgaagttcttagc 60
 Db 5 CTTTGAAGCATTTTGTCTGTCTGCTCCCTGATCTTCAGGTACCACTGAGTTCTTAGC 64
 OY 61 agtccgtgactccttgggaattccactcttctgctcctgcccagaatccgaacaagc 120
 Db 65 AGTCTGTGACTCTTGGAGTTTCATCTTGTGCTCTGCCAGAAATCGCAACAGC 124
 OY 121 tgcctcagctgcaacgatacctgactgctcctgctgctgatagaagaagccctgaatgctga 180
 Db 125 TGTCTCAGCTGACAGTATCAGTACTGTCTGCTGATGATGAACCCCTGATGCTGA 184
 OY 181 aaccactgctgctgcaacaactggaacactgctgctcctcaccactggaacacacgctgc 240
 Db 185 AACCACTGCTGCTGCAACCACTGCGACCACTGCTGCTCTTACCACTGCAACCGCTGC 244
 OY 241 ttctaccactgctgctgaagaacatltccagtttaccccaatgggttgggagatcccgaa 300
 Db 245 TTCTACCACTGCTGCTGAAGACATTCAGTTTACCCAAATGGGTTGGGATCTTCCGAA 304
 OY 301 tggc 304
 Db 305 TGGT 308

RESULT 12

AX240677

LOCUS AX240677 292 bp DNA linear PAT 26-SEP-2001
 DEFINITION Sequence 3 from Patent WO0165262.
 ACCESSION AX240677
 VERSION AX240677.1 GI:15797660
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 292)

AUTHORS Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., and Stroppe, S.D.
TITLE Reagents and methods useful for detecting diseases of the breast
JOURNAL Patent: WO 0165262-A 3 07-SEP-2001;
ABBOTT LABORATORIES (US)
FEATURES
source location/Qualifiers
1. .292
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="EST Clone 901429"
BASE COUNT 59 a 92 c 59 g 80 t 2 others
ORIGIN
Query Match 60.9%; Score 286.8; DB 6; Length 292;
Best Local Similarity 98.6%; Pred. No. 4.6e-58;
Matches 288; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 8 gcatattgtctgtcctccatcgaagtcacacacatgaagttcttagcaagtcctg 67
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Db 1 GCATTTTGTCTGTGCTCCCTGATCTTCATGTACACACCATGAAGTTCTTAGCAGTCTG 60
OY 68 gtaactcttggaagttccatcttctgtctctgcccgaatccgaacagctgctcca 127
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Db 61 GTACTCTTGGAGTTTCATCTTCTGTCTCTGCCAGAAATCCGACACAGCTGCTCCA 120
OY 128 gctgaacagatccagctactgtctctgtctgaatgaagccctgtagtctgaacact 187
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Db 121 GCTGACAGGTATCCAGCTACTGCTGCTGATGATGAAGCCCTGATGTGAACCACT 180
OY 188 gctctcaaaaactgagacacactgctgctctctcaactgaacacacgctgcttacc 247
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Db 181 GCTCTGCACACCTGCGACACCTGCTCTCTCACTGACACACCGCTGCTTATAC 240
OY 248 actgctcgtaaaagacatccagtttaccacaaatgggttggaagttcccca 299
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Db 241 ACTGCTGTAAGACATTNCGTTTACCCAAATGGGTGGAGATCTCCCA 292
RESULT 13
AX328499 273 bp DNA linear PAT 07-JAN-2002
LOCUS AX328499 Sequence 2 from Patent WO0135811.
DEFINITION AX328499
ACCESSION AX328499
VERSION AX328499.1 GI:18098425
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE Mack, D. and Gish, K.C.
TITLE Novel methods of diagnosing and determining prognosis of breast
cancer, compositions, and methods of screening for breast cancer
modulators
JOURNAL Patent: WO 0135811-A 2 25-MAY-2001;
EOS Biotechnology, Inc. (US)
FEATURES
source location/Qualifiers
1. .273
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 58 a 85 c 59 g 71 t
ORIGIN
Query Match 57.3%; Score 269.8; DB 6; Length 273;
Best Local Similarity 99.3%; Pred. No. 5.1e-54;
Matches 271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 47 atgaagttcttaacagctccggaacacctggagagttcattcttctgtctctccag 106
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Db 1 ATGAAGTTCTTACAGCTCGTACTCTTGGAGTTTCATCTTCTGTGCTCTGCCAG 60

OY 107 aatccgaacagctgtctccagctgagcaagatattccagctactgtctctgtatgaatga 166
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Db 61 AATCCGACACAGCTGTGCCAGCTGACACGATTCACACTGTCTGTCTGTGATGATCA 120
OY 167 gccctgtatgtgaacacactgtctgctgaacaaactgaacacactgtctcttacc 226
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Db 121 GCCCTGATGCTGAACACACTGCTGTGCAACCACTGCAACACTGCTGCTTACTACT 180
OY 227 gcaacacacgctgtcttaccactgtctgtaagacattccagtttaccacaaatggt 286
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Db 181 GCAACACACGCTGCTTCTTACACACTGCTGTAAAGACATTCAGTTTACCAATGAGCTT 240
OY 287 gggatctccgaatgtagatgtgtccctga 319
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Db 241 GGGATCTCCGAAATGTTAGATGTGTCTCCCTGA 273
RESULT 14
AX079476 264 bp DNA linear PAT 22-FEB-2001
LOCUS AX079476 Sequence 220 from Patent WO0107611.
DEFINITION AX079476
ACCESSION AX079476
VERSION AX079476.1 GI:13159036
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE Baker, K.P., Goddard, A. and Wood, W. I.
TITLE Human polypeptides and methods for the use thereof
JOURNAL Patent: WO 0107611-A 220 01-FEB-2001;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
1. .264
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 54 a 87 c 53 g 70 t
ORIGIN
Query Match 54.3%; Score 255.6; DB 6; Length 264;
Best Local Similarity 98.5%; Pred. No. 1.2e-50;
Matches 258; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 cttgaagcaattttgtctgtgtctccatctcagctcagacacacccaagaattcttacc 60
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Db 3 CTTTGAAGCACTTTTGTGTGTCTGCTGCTGATCTTCAAGTACCCCATGAAGCTTTTAC 62
OY 61 agtccgtgtaactcttggaattcattcttctgtctgtcgtccagaatccgaacacac 120
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Db 63 AGTCTGTACTCTTGTGGAGTTTCCATCTTGTGCTCTGCCCAATCCGACAAACAC 122
OY 121 tgtctcagctggaagatccagctactgtctgtctgtatgaagacccctgaatga 180
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Db 123 TGCTCCAGCTGACACGATTCACACTGCTGCTCTGATGAAGACCCCTGATGCTGA 182
OY 181 aaccactgtctgtcaacaaactgagacacactgtctgtcttaccactgaacacacac 240
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Db 183 AACCACTGCACTGCAACCACTGCGACCACTGCTGCTTACTACTGCAACCACTGCT 242
OY 241 ttctaccactgtctgtaagaac 262
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Db 243 TTCTTACTACTGCTGTAAGAC 264
RESULT 15
AX079475 266 bp DNA linear PAT 22-FEB-2001
LOCUS AX079475 Sequence 219 from Patent WO0107611.
DEFINITION AX079475
ACCESSION AX079475
VERSION AX079475.1 GI:13159035

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 266)
JOURNAL Baker, K.P., Goddard, A. and Wood, W.I.
Human polypeptides and methods for the use thereof
Patent: WO 0107611-A 219 01-FEB-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..266
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 54 a 88 c 54 g 70 t
ORIGIN

Query Match 54.3%; Score 255.6; DB 6; Length 266;
Best Local Similarity 98.5%; Pred. No. 1.2e-50;
Matches 258; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 61 agtcctgtactcttggaagttccatcttctgtctctgtccagaatccgaacaagc 120
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Db 65 agtcctgtactcttggaagttccatcttctgtctctgtccagaatccgaacaagc 124
QY 121 tgcacagctgacagcatalccagctactggtctgtctgatlgaagccctgatlgtga 180
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Db 125 tgcacagctgacagcatalccagctactggtctgtctgatlgaagccctgatlgtga 184
QY 181 aaccactgctgctgacacaaactgacacactgctgcttccactgacacacacgctgc 240
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Db 185 aaccactgctgac 244
QY 241 tctaccactgctgctgacacacacacacacacacacacacacacacacacacac 262
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Db 245 tctaccactgctgctgacacacacacacacacacacacacacacacacacacac 266

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